

Figure 1

1	GCTGAACAGACAGAAGAAATCACTTGAATGCTGGGGACATCACCTACTCTGTCCGGGCCATG	60
1	AlaGluGlnThrArgAsnHisLeuAsnAlaGlyAspIleThrTyrSerValArgAlaMet	20
61	GACCAGCTGGTAGGCCTCCTAGATGTACAGCTTCGGAACCTTGACCCAGGTGGAAAAGAT	120
21	AspGlnLeuValGlyLeuLeuAspValGlnLeuArgAsnLeuThrProGlyGlyLysAsp	40
121	AGTGCTGCCCCGAGTTTGAACAAGGCAATGGTCGAGACAGTTAACAACCTCCTTCAGCCA	180
41	SerAlaAlaArgSerLeuAsnLysAlaMetValGluThrValAsnAsnLeuLeuGlnPro	60
181	CAAGCTTTGAATGCATGGAGAGACCTGACTACGAGTGATCAGCTGCGTGGGCCACCATG	240
61	GlnAlaLeuAsnAlaTrpArgAspLeuThrThrSerAspGlnLeuArgAlaAlaThrMet	80
241	TTGCTTCATACTGTGGAGGAAAGTGCTTTTGTGCTGGCTGATAACCTTTTGAAGACTGAC	300
81	LeuLeuHisThrValGluGluSerAlaPheValLeuAlaAspAsnLeuLeuLysThrAsp	100
301	ATTGTCAGGGAGAATACAGACAATATTAAATTGGAAGTTGCAAGACTGAGCACAGAAGGA	360
101	IleValArgGluAsnThrAspAsnIleLysLeuGluValAlaArgLeuSerThrGluGly	120
361	AACTTAGAAGACCTAAAAATTTCCAGAAAACATGGGCCATGGAAGCACTATCCAGCTGTCT	420
121	AsnLeuGluAspLeuLysPheProGluAsnMetGlyHisGlySerThrIleGlnLeuSer	140
421	GCAAAATACCTTAAAGCAAAATGGCCGAAATGGAGAGATCAGAGTGGCCTTTGTCTGTAT	480
141	AlaAsnThrLeuLysGlnAsnGlyArgAsnGlyGluIleArgValAlaPheValLeuTyr	160
481	AACAACCTGGGTCTTATTATCCACGGAGAATGCCAGTATGAAGTTGGGAACGGAAGCT	540
161	AsnAsnLeuGlyProTyrLeuSerThrGluAsnAlaSerMetLysLeuGlyThrGluAla	180
541	TTGTCCACAAATCATCTCTGTATTGTCAATTCCCTGTTATTACGGCAGCAATAACAAA	600
181	LeuSerThrAsnHisSerValIleValAsnSerProValIleThrAlaAlaIleAsnLys	200
601	GAGTTTCAGTAACAAGGTTTATTGGCTGATCCTGTGGTATTTACTGTAAACATATCAAG	660
201	GluPheSerAsnLysValTyrLeuAlaAspProValValPheThrValLysHisIleLys	220
661	CAGTCAGAGGAAAATTTCAACCCTAACTGTTCATTTTGGAGCTACTCCAAGCGTACAATG	720
221	GlnSerGluGluAsnPheAsnProAsnCysSerPheTrpSerTyrSerLysArgThrMet	240
721	ACAGGTTATTGGTCAACACAAGGCTGTGGCTCCTGACAACAAATAAGACACATACTACA	780
241	ThrGlyTyrTrpSerThrGlnGlyCysArgLeuLeuThrThrAsnLysThrHisThrThr	260
781	TGCTCTTGTAACCACCTAACAAATTTGTCAGTACTGATGGCAGTGTGGAAGTTAAGCAC	840
261	CysSerCysAsnHisLeuThrAsnPheAlaValLeuMetAlaHisValGluValLysHis	280
841	AGTGATGGCGGTCCATGACCTCCTTCTGGATGTGATCAGCTGGGTGGAATTTTGCTGTCC	900
281	SerAspAlaValHisAspLeuLeuLeuAspValIleThrTrpValGlyIleLeuLeuSer	300
901	CTTGTTTGTCTCCTGATTGTGATCTTCACATTTTGCTTTTCCGGGGCTCCAGAGTGAC	960
301	LeuValCysLeuLeuIleCysIlePheThrPheCysPhePheArgGlyLeuGlnSerAsp	320
961	CGTAACACCATCCACAGAACCCTCTGCATCAGTCTCTTTGTAGCAGAGCTGCTCTTCCTG	1020
321	ArgAsnThrIleHisLysAsnLeuCysIleSerLeuPheValAlaGluLeuLeuPheLeu	340
1021	ATTGGGATCAACCGAAGTACCAACCAATGGCTGTGCTGTTTTGCTGCCCTGTTACAT	1080
341	IleGlyIleAsnArgThrAspGlnProIleAlaCysAlaValPheAlaAlaLeuLeuHis	360
1081	TTCTTCTTCTTGCTGCTTCACCTGGATGTTCTCGAGGGGTGCAGCTTTATATCATG	1140
361	PhePhePheLeuAlaAlaPheThrTrpMetPheLeuGluGlyValGlnLeuTyrIleMet	380
1141	CTGGTGGAGGTTTTTGGAGAGTGAACATTCACGTAGGAAATACTTTTATCTGGTGGCTAT	1200
381	LeuValGluValPheGluSerGluHisSerArgArgLysTyrPheTyrLeuValGlyTyr	400
1201	GGGATGCCCTGCACTCATTGTGGCTGTGTACCTGCAGTAGACTACAGGAGTTATGGAACA	1260
401	GlyMetProAlaLeuIleValAlaValSerAlaAlaValAspTyrArgSerTyrGlyThr	420
1261	GATAAAGTATGTTGGCTCCGACTTGACACCTACTTCATTTGGAGTTTTATAGGACCAGCA	1320
421	AspLysValCysTrpLeuArgLeuAspThrTyrPheIleTrpSerPheIleGlyProAla	440
1321	ACTTTGATAATTATGCTTAATGTAATCTTCCTTGGGATTGCTTTATATAAAATGTTTCAT	1380
441	ThrLeuIleIleMetLeuAsnValIlePheLeuGlyIleAlaLeuTyrLysMetPheHis	460
1381	CATACTGCTATACTGAAACCTGAATCAGGCTGCTCTTGATAACATCAAGTCATGGGTTATA	1440
461	HisThrAlaIleLeuLysProGluSerGlyCysLeuAspAsnIleLysSerTrpValIle	480
1441	GGTGCAATAGCTCTTCTCTGCCTATTAGGATTGACCTGGGCTTTGGACTCATGTATATT	1500
481	GlyAlaIleAlaLeuLeuCysLeuLeuGlyLeuThrTrpAlaPheGlyLeuMetTyrIle	500

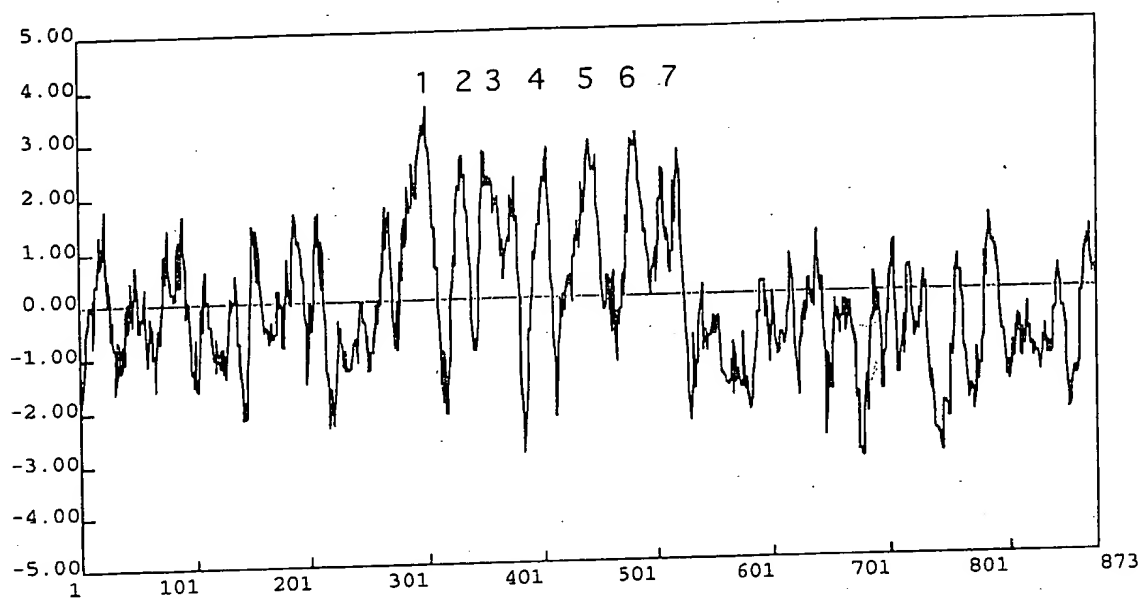
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Figure 2

1501 AATGAAAGCACAGTCATCATGGCCTATCTCTTACCATTTCATTTCTCTACAGGGAATG 1560
 501 AsnGluSerThrValIleMetAlaTyrLeuPheThrIlePheAsnSerLeuGlnGlyMet 520
 1561 TTTATATTTATTTTCCATTGTGTCTTACAGAAGAAGGTACGAAAAGAGTATGGGAAATGC 1620
 521 PheIlePheIlePheHisCysValLeuGlnLysLysValArgLysGluTyrGlyLysCys 540
 1621 CTGCGAACACATTGCTGTAGTGGCAAAAGTACAGAGAGTTCCATTGGTTCAGGGAAAACA 1680
 541 LeuArgThrHisCysCysSerGlyLysSerThrGluSerSerIleGlySerGlyLysThr 560
 1681 TCTGGTTCTCGAACTCCTGGACGCTACTCCACAGGCTCAGAGAGCCGAATCCGTAGAATG 1740
 561 SerGlySerArgThrProGlyArgTyrSerThrGlySerGlnSerArgIleArgArgMet 580
 1741 TGAATGACACGGTTCGAAAGCAGTCAGAGTCTTCTTTTATTACTGGAGACATAAACAGT 1800
 581 TrpAsnAspThrValArgLysGlnSerGluSerSerPheIleThrGlyAspIleAsnSer 600
 1801 TCAGCGTCACTCAACAGAGAGGGGCTTCTGAACAATGCCAGGGATACAAGTGTCTATGGAT 1860
 601 SerAlaSerLeuAsnArgGluGlyLeuLeuAsnAsnAlaArgAspThrSerValMetAsp 620
 1861 ACTCTACCACTGAATGGTAACCATGGCAATAGTTACAGCATTGCCAGCGCGAATACCTG 1920
 621 ThrLeuProLeuAsnGlyAsnHisGlyAsnSerTyrSerIleAlaSerGlyGluTyrLeu 640
 1921 AGCAACTGTGTGCAATCATAGACCGTGGCTATAACCATAACGAGACCGCCCTAGAGAAA 1980
 641 SerAsnCysValGlnIleIleAspArgGlyTyrAsnHisAsnGluThrAlaLeuGluLys 660
 1981 AAGATTCTGAAGGAATCACTTCCAATATATCCCTTCTTACCTGAACAACCATGAGCGC 2040
 661 LysIleLeuLysGluLeuThrSerAsnTyrIleProSerTyrLeuAsnAsnHisGluArg 680
 2041 TCCAGTGAACAGAACAGGAATCTGATGAACAAGCTGGTGAATAACCTTGGCAGTGGAGG 2100
 681 SerSerGluGlnAsnArgAsnLeuMetAsnLysLeuValAsnAsnLeuGlySerGlyArg 700
 2101 GAAGATGATGCCATTGTCTGGATGATGCCACCTCGTTTAAACCAGGAGAGTTTGGGC 2160
 701 GluAspAspAlaIleValLeuAspAspAlaThrSerPheAsnHisGluGluSerLeuGly 720
 2161 CTGGAACCTCATTATGAGGAATCTGATGCTCTCTTGTGCCCCAAGAGTATACTCCACC 2220
 721 LeuGluLeuIleHisGluGluSerAspAlaProLeuLeuProProArgValTyrSerThr 740
 2221 GAGAACCACAGCCACACCAATTATACCAGAAGGCGGATCCCCAAGACCACAGTGAGAGC 2280
 741 GluAsnHisGlnProHisHisTyrThrArgArgArgIleProGlnAspHisSerGluSer 760
 2281 TTTTTCCTTTGTCTAACCAACGAGCACACAGAAGATCTCCAGTCACCCCATAGAGACTCT 2340
 761 PhePheProLeuLeuThrAsnGluHisThrGluAspLeuGlnSerProHisArgAspSer 780
 2341 CTCTATACCAGCATGCCGACACTGGCTGGTGTGGCCGCCACAGAGAGTGTACCACCAGC 2400
 781 LeuTyrThrSerMetProThrLeuAlaGlyValAlaAlaThrGluSerValThrThrSer 800
 2401 ACCCAGACCGAACCCCCACCGCCAAATGTGGTGTGCGGAAGATGTTTACTACAAAAGC 2460
 801 ThrGlnThrGluProProProAlaLysCysGlyAspAlaGluAspValTyrTyrLysSer 820
 2461 ATGCCAAACCTAGGCTCCAGAAACCAGTCCATCAGCTGCATACTTACTACCAGCTAGGT 2520
 821 MetProAsnLeuGlySerArgAsnHisValHisGlnLeuHisThrTyrTyrGlnLeuGly 840
 2521 CGCGGCAGCAGTGTGATTTATAGTTCTTCCAAACAAAGATGGGACCCCTCCGAGGGA 2580
 841 ArgGlySerSerAspGlyPheIleValProProAsnLysAspGlyThrProProGluGly 860
 2581 AGTTCAAAAGGACCGGCTCATTGGTCACTAGTCTATAGAAGATGACACAGAAATTGGAA 2640
 861 SerSerLysGlyProAlaHisLeuValThrSerLeu*** 873
 2641 CCAACAAAACCTGCTAACACCTTGTGACTGTTCTGAGTTGATATAAGCAGTGGTAATAAT 2700
 873 873
 2701 GTGTGTACTCTAAATCTTTATGTCTCTCTTAAAGACAAACAAAACCTCTCAGACTTTT 2760
 873 873
 2761 TTTTTTTTTTAAATGGGATTTTATAGTCTAGCCAGGGGAGAAAGATAACTGCTAAAATTCCT 2820
 873 873
 2821 CTGTACCCGATCCTTTCTTGTCTTTCCCTTCAGATGGAGACTTCATTATGTTAATGAA 2880
 873 873
 2881 CAAGATATGAAGAAATGGCACTCATTGTGGCTTGTGAATTATGTTGTATGTTTAA 2940
 873 873
 2941 ACATCTCTGATGCTGTGTTACTAAAATTACAAGGACCTGCTTTTTAAAGGCCAGAACAA 3000
 873 873

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Figure 3



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[illegible]

	- - - -	E G S K G T K P P A V S T T K I P P I T N I F P L P E R F C E A L D \$ K G I K W P Q T O R G M M Y	HK05006 HK05490
1	- - - -	- - - -	- - - -
51	- - - -	E R P C P K G T R G T A S Y L C M I S T G T W N P K G P D L S N C T S H W V N O L A Q K I R S G E N	HK05006 HK05490
1	- - - -	A E Q T R N H L N A G D I T Y S V R A M D Q L V G L L D V Q L R N L T P G G K D S A	HK05006
101	- - - -	A A S L A N E L A N K H T K G P V F A G D V S S V R L M E Q L V D I L D A O L O E L K P E S E K D S A	HK05490
43	- - - -	A R S L N K - - - - - A M V E T V N N L L Q P O A L N A W R D L T T S D Q L R A A T	HK05006
151	G R S Y N K L O K R E K T C R A Y L K A I V D T Y D N L L R P E A L E S W K H M N S S E Q A H T A T	HK05490	
80	M L I H T V E E S A F V L A D N L L K T D D I V R E N T D N I K L E V A R L S T E G N L E D L K F P E	HK05006	
201	M L L D T L E E G A F V L A D N L L E P T R V S M P T E N I V L E V A Y L S T E G Q I Q D F K F P L	HK05490	
130	N H - G H C S T I Q L S A N T L K Q N G R N G E I R V A F V L Y N N L G P Y L S T E N A S M K L G T	HK05006	
251	G I K G A G S S I O L S A N T V K O N S R N G L A K L V F I I Y R S L G O F L S T E N A T I K L G A	HK05490	
179	E A J S T N H S V I V N S P V I T A A I N K E F S N K V Y L A D P V V F T V K X H I K Q S E N F N P	HK05006	
301	D F I G R N S T I A V N S H V I S V S I N K E - S S R V Y L T D P V L F T L P H I - D P D N Y F N A	HK05490	
229	N C S F W S Y S K R T M T G Y W S T Q G C R L L T T N K T H T T C S C N H L T N F A V L M A H V E V	HK05006	
349	N C S F W N Y S E R T M M G Y W S T Q G C K L V D T N K T R T T C A C S H L T N F A I L M A H R E I	HK05490	
279	K H S D A V H D L L L D V I T W V G I L L S L V C L L I C I F T F C F F R G L Q S D R N T I H K N L	HK05006	
359	A Y K D G V H E L L L T V I T W V G I V I S L V C L A I C I F T F C F F R G L Q S D R N T I H K N L	HK05490	
329	C I S L F V A E L L F L I G I N R T D Q P I A C A V F A L L H F F F L A A F T W M F L E G V Q L Y	HK05006	
449	C I N L E I A B F I F L I G I D K T K Y A I A C P I F A G L L H F F F L A A F A W M C L E G V Q L Y	HK05490	
379	I M L V E V F E S E H S R R K Y F Y L V G Y G M P A L I V A V S A A V D Y R S Y G T D K V C W L R L	HK05006	
499	L M L V E V F E S E Y S R K K Y Y Y V A G Y L F P A T V V G V S A I D Y K S Y G T E K A C N L H V	HK05490	

Figure 5

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423	D T Y F I W S F I G P A T L I I M L N V I F L G I A L Y K K M F H H T A I L K P E S G C L D N I K S W	HK05006
549	D N Y F I W S F I G P V T F I I L L N I I F L V I T L C K M V K H S N T L K P D S S R L E N I K S W	HK05490
479	V I G A I A L L C L L G L T W A F G L M Y I N E S T V I M A Y L F T I F N S L Q G M F I F I F H C V	HK05006
599	V L G A F A L L C L L G L T W S F G L L F I N E T I V M A Y L F T I F N A F Q G V F I F I F H C A	HK05490
529	L Q K K V R K E Y G K C L R - T H C C S G K S T E S S I G S G K T S G S R T P G R Y S T G S Q S R I	HK05006
649	L Q K K V R K E Y G K C F R H S Y C C G G L P T E S P H S S V K A S T T R T S A R Y S S G T Q S R I	HK05490
578	R R M W N D T V R K Q S E S S F I T G D I N S S A S L N R E G L - - - - - - - - - - - - - - - -	HK05006
699	R R M W N D T V R K Q S E S S F I S G D I N S T S T L N - Q G M T G N Y L L T N P L L R P H G T N N	HK05490
610	- -	HK05006
748	P Y N T L L A E T V V C N A P S A P V F N S P G H S L N N A R D T S A M D T L P L N G N F N N S Y S	HK05490
534	I A S G E Y L S N C V Q I I D R G Y N H N E T A L E K K I L K E L T S N Y I P S Y L N N H E R S S E	HK05006
798	L H K G D Y - N D S V Q V Y D C G L S L N D T A F E K M I I S E L - - - - - - - - - - - - - - - -	HK05490
584	C N R N L K N K L V N N - - L G S G R E D D A I V L D D A T S F N H E S L G L E L I H E E S D A P	HK05006
839	K T H N L E L T I P V K P V I G G S S E D D A I V A D A S S L M H S D N P G L E L H H K E L E A P	HK05490
732	L L P P R V Y S T E N H Q P H Y T R R R I P Q D H S E S E F P L L T N E H T E D L Q S P H R D S L	HK05006
889	L I P O R T H S L L - Y Q P Q - - - - - K K V K S E G T D S Y V S Q L T A E A E D H L O S P N R D S L	HK05490
782	Y T S M P P T L A G V A A T E S V T T S T Q T E P P P A K C G D A E D V Y Y K S M P N L G S R N N H V H	HK05006
934	Y T S M P P N L R D S P Y P E S - S P D M E E D L S P S R R S E N E D I Y Y K S M P N L G A - - - G H	HK05490
832	Q L H T Y Y Q L G R G S S D C F I V P P N K D G T P P E C S S K - G P A H L V T S L	HK05006
980	Q L Q M C Y Q I S R G N S D G Y I I P I N K E G C I P E C D V R E G O M Q L V T S L	HK05490

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Figure 6

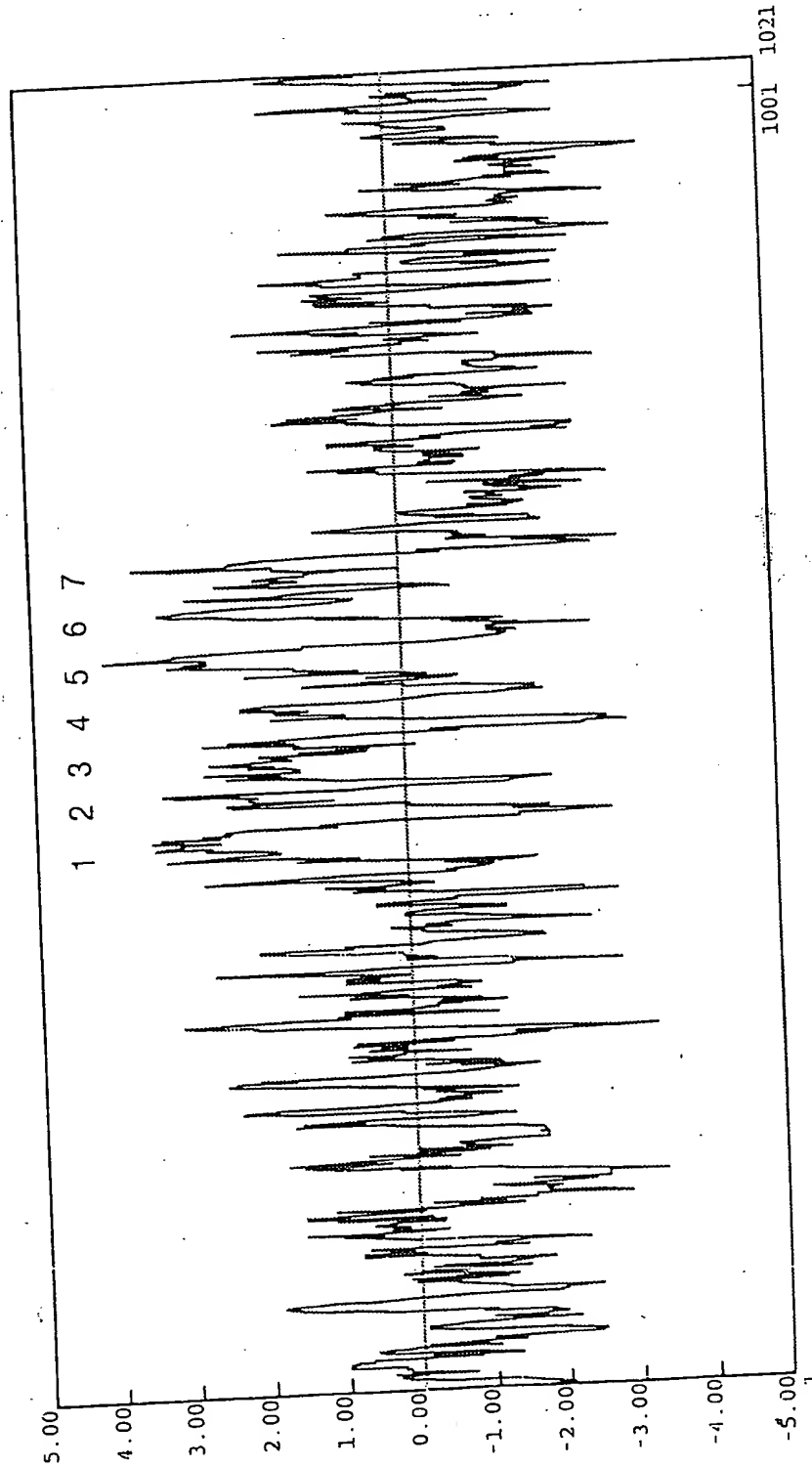


Figure 7

1	GAAGGAAGCAAGGACAAACACCTCCAGCAGTTTCTACCAACCAAAATTCACCTATA	60
1	GlulysSerLysGlyThrLysProProAlaValSerThrThrLysIleProProIle	20
61	ACAAATATTTTCCCTCCAGAGAGATTCTGTGAAGCAATTAGACTCCAGGGGATAAAG	120
21	ThrAsnIlePheProLeuProGluArgPheCysGluAlaLeuAspSerLysGlyIleLys	40
121	TGGCCTCAGACACAAAGGGGAATGATGTTGAACCACTATGCCCTAAGGGAACAAGAGA	180
41	TripProGlnThrGlnArgGlyMetMetValGluArgProCysProLysGlyThrArgGly	60
181	ACTGCTCATATCTCTGCATGATTTCCACTGGAACATGGAACCTTAAGGCCCCGATCTT	240
61	ThrAlaSerTyrLeuCysMetIleSerThrGlyThrTyrAsnProLysGlyProAspLeu	80
241	AGCAACTGTACCTCACACTGGTCAATCAGCTGGCTCAGAAGATCAGAAGCGGAGAAAT	300
81	SerAsnCysThrSerHisTyrValAsnGlnLeuAlaGlnLysIleArgSerGlyGluAsn	100
301	GCTGCTAGTCTTGCCATGAAGTGGCTAAACATACCAAGGGCCAGTGTTCCTGGGAT	360
101	AlaAlaSerLeuAlaAsnGluLeuAlaLysHisThrLysGlyProValPheAlaGlyAsp	120
361	GTAAGTCTTCAGTGAGATTGATGGAGCAGTGGTGGACATCCTTGATGCCACAGCTGCAG	420
121	ValSerSerSerValArgLeuMetGluGlnLeuValAspIleLeuAspAlaGlnLeuGln	140
421	GAAGTGAACCTAGTGAAAAGATTTCAGCTGGACGGAGTTATAACAGCTCCAAAACGA	480
141	GluLeuLysProSerGluLysAspSerAlaGlyArgSerTyrAsnLysLeuGlnLysArg	160

Figure 8

481 GAGNAGACATGCGGGCTTACCTTAAGCAATTGTGACACAGTGGACAACCTTCGAGA 540
161 GluLysThrCysArgAlaTyrLeuLysAlaIleValAspThrValAspAsnLeuLeuArg 180

541 CCTGAAGCTTTGGAAATCATGGAACATATGAATTCCTTCTGAACAAGCACATACGCAACA 600
181 ProGluAlaLeuGluSerTrpLysHisMetAsnSerSerGluGlnAlaHisThrAlaThr 200

601 ATGTTACTCGATACATGGAAGAGGAGCTTTGTCTCTAGCTGACAAATCCTTTAGAACCA 660
201 MetLeuLeuAspThrLeuGluGluGlyAlaPheValLeuAlaAspAsnLeuLeuGluPro 220

661 ACAAGGGTCTCAATGCCACAGAAATATTTGTCCTGGAGTTGCCGTACTCAGTACAGAA 720
221 ThrArgValSerMetProThrGluAsnIleValLeuGluValAlaValLeuSerThrGlu 240

721 CGACAGATCCAAGACTTTAAATTTCTCTGGCATCAAGGAGCAGGAGCTCAATCCAA 780
241 GlyGlnIleGlnAspPheLysPheProLeuGlyIleLysGlyAlaGlySerSerIleGln 260

781 CTGTCCGCAATACCGTCAACAGAACAGCAGGAATGGGCTTGCMAAGTTGGTGTTCATC 840
261 LeuSerAlaAsnThrValLysGlnAsnSerArgAsnGlyLeuAlaLysLeuValPheIle 280

841 ATTTACCGGAGCTGGACAGTTCTCTTAGTACAGAAATGCAACCATTAACCTGGTGCT 900
281 IleTyrArgSerLeuGlyGlnPheLeuSerThrGluAsnAlaThrIleLysLeuGlyAla 300

901 GATTTATTTGTTGTAATAGCACCAATTCAGTGAACCTCAGTCAATTCAGTTTCAATC 960
301 AspPheIleGlyArgAsnSerThrIleAlaValAsnSerHisValIleSerValSerIle 320

961 AATAAGAGTCCAGCCGAGTATACCTGACTGATCTGTGCTTTTACCCCTGCCACACATT 1020

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Figure 9

321 AsnLysGluSerSerArgValTyrLeuThrAspProValLeuPheThrLeuProHisIle 340
1021 GATCCTGACAATTATTTCAATGCAAACTGCTCTCTGGAACACTACACAGAGAACTATG 1080
341 AspProAspAsnTyrPheAsnAlaAsnCysSerPheTrpAsnTyrSerGluArgThrMet 360
1081 ATGGGATATTGCTCTACCCAGGGCTGCAAGCTGGTTGACACTAATAAACTCGAACACG 1140
361 MetGlyTyrTrpSerThrGlnGlyCysLysLeuValAspThrAsnLysThrArgThrThr 380
1141 TGTGATGCAGCCACCTAACCAATTTTGGCAATCTCATGCCCACAGGAAATTCATAT 1200
381 CysAlaCysSerHisLeuThrAsnPheAlaIleLeuMetAlaHisArgGluIleAlaTyr 400
1201 AAAGATGGCGTTCATGATTAATCTCTTACAGTCATCACCTGGGTCGGAATGTCTATTC 1260
401 LysAspGlyValHisGluLeuLeuLeuThrValIleThrTrpValGlyIleValIleSer 420
1261 CTTGTTTCCTGGCTATCTGCATCTTCACCTTCCTGCTTTTCGGTGGCTACAGAGTGAC 1320
421 LeuValCysLeuAlaIleCysIlePheThrPheCysPhePheArgGlyLeuGlnSerAsp 440
1321 CGAAATACTATTCACAAGAACCTTTGTATCAACCTTTTCATTCGCTGAATTTTCCTA 1380
441 ArgAsnThrIleHisLysAsnLeuCysIleAsnLeuPheIleAlaGluPheIlePheLeu 460
1381 ATAGGCATTGATAAGACAAAATATGCGATTGATGCCCAATATTTGCAGGACTTCTACAC 1440
461 IleGlyIleAspLysThrLysTyrAlaIleAlaCysProIlePheAlaGlyLeuLeuHis 480

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Figure 10

1441 TTTTCTTTTGGCAGCTTTTGCTTGGATGTGCTAGAAAGGTGTGCAGCTCTACCTAATG 1500
 481 PhePhePheLeuAlaAlaPheAlaTrpMetCysLeuGluGlyValGlnLeuTyrLeuMet 500
 1501 TTAGTTGAAGTTTTTGAAAGTGAATATTCAAGGAAAAAATATTACTATGTTGCTGGTTAC 1560
 501 LeuValGluValPheGluSerGluTyrSerArgLysLysTyrTyrTyrValAlaGlyTyr 520
 1561 TTGTTTCTGCCACAGTGGTTGGAGTTTCAGCTGCTATTGACTATAAGAGCTATGGAACA 1620
 521 LeuPheProAlaThrValValGlyValSerAlaAlaIleAspTyrLysSerTyrGlyThr 540
 1621 GAAAAAGCTTGCTGGCTTCATGTTGATAACTACTTTATATGGAGCTTCATTGGACCTGTT 1680
 541 GluLysAlaCysTrpLeuHisValAspAsnTyrPheIleTrpSerPheIleGlyProVal 560
 1681 ACCTTCATTATTCTGCTAAATATTATCTTCTTGCTGATCACATTGTGCAAAATGGTGAAG 1740
 561 ThrPheIleIleLeuLeuAsnIleIlePheLeuValIleThrLeuCysLysMetValLys 580
 1741 CATTCAAACACTTTGAAACCAGATTCTAGCAGGTTGGAAAACATTAAAGTCTTGGGTGCTT 1800
 581 HisSerAsnThrLeuLysProAspSerSerArgLeuGluAsnIleLysSerTrpValLeu 600
 1801 GGCGCTTTGCTCTTCTGTGTCTTCTTGGCCTCACCTGGTCCTTTGGGTGCTTTTTATT 1860
 601 GlyAlaPheAlaLeuLeuCysLeuLeuGlyLeuThrTrpSerPheGlyLeuLeuPheIle 620
 1861 AATGAGGAGACTATTGTGATGGCATATCTCTTCACTATATTTAATGCTTTCCAGGGAGTG 1920
 621 AsnGlnGluThrIleValMetAlaTyrLeuPheThrIlePheAsnAlaPheGlnGlyVal 640
 1921 TTCATTTTCATCTTTCACTGTGCTCTCCAAAAGAAAGTACGAAAAGATATGGCAAGTGC 1980
 641 PheIlePheIlePheHisCysAlaLeuGlnLysLysValArgLysGluTyrGlyLysCys 660

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Figure 11

1981 TTCAGACATCATCTGCTGTGGAGGCTCCCAACTCAGAGTCCCCACAGTTCAGTGAAG 2040
661 PheArgHisSerTyrCysGlyGlyLeuProThrGluSerProHisSerSerVallys 680
2041 GCATCAACACCAGAACCCAGTGTCTGGCTATTCTCTCTGGCACACAGAGTCGTATAAGAAGA 2100
681 AlaSerThrThrArgThrSerAlaArgTyrSerSerGlyThrGlnSerArgIleArgArg 700
2101 ATGTGGAAATGATCTGTGAGAAACAATCAGATCTCTCTTTTATCTCAGGTGACATCAAT 2160
701 MetTrpAsnAspThrValArgLysGlnSerGluSerSerPheIleSerGlyAspIleAsn 720
2161 AGCACTTCAACACTTAATCAAGGAATGACTGGCAATTACCTACTAACAACCCCTCTTCTT 2220
721 SerThrSerThrLeuAsnGlnGlyMetThrGlyAsnTyrLeuLeuThrAsnProLeuLeu 740
2221 CGACCCCAAGGCACTAACAACCCCTATATACACATCTGCTGCTGAAACAGTTGTATGTAAAT 2280
741 ArgProHisGlyThrAsnAsnProTyrAsnThrLeuLeuAlaGluThrValValCysAsn 760
2281 GCCCCTTCAGCTCCTGTATTAACTCACCAGGACATTCACCTGAACAATGCCAGGGATACA 2340
761 AlaProSerAlaProValPheAsnSerProGlyHisSerLeuAsnAlaArgAspThr 780
2341 AGTGCCATGGATCTCTACCGCTAAATGGTAATTTTAAACACAGCTACTCGCTGCACAAG 2400
781 SerAlaMetAspThrLeuProLeuAsnGlyAsnPheAsnAsnSerTyrSerLeuHisLys 800
2401 GGTGACTATAATGACACGGTGCAGTTGTGGACTGTGGACTAAGTCTGAATGATAGTCTGT 2460
801 GlyAspTyrAsnAspSerValGlnValValAspCysGlyLeuSerLeuAsnAspThrAla 820

Figure 12

2461 TTGAGAAATGATCAATTCAGAATTAGTGACAACAACITACGGGGCAGCAGCAAGACT 2520
821 PheGluLysMetIleIleSerGluLeuValHisAsnAsnLeuArgGlySerSerLysThr 840

2521 CACAACCTCGAGCTCAGGCTACCGCTACAGTCAACCTGTGATTGGAGGTAGCAGCAGTGAAGAT 2580
841 HisAsnLeuGluLeuThrLeuProValLysProValIleGlyGlySerSerSerGluAsp 860

2581 GATGCTATTGTGGCAGATGCTTCATCTTTAATGCACAGCGACAACCCAGGGCTGGAGCTC 2640
861 AspAlaIleValAlaAspAlaSerSerLeuMetHisSerAspAsnProGlyLeuGluLeu 880

2641 CATCACAAGAACTCGAGGCCACCTTATTCCTCAGCGGACTCCTCCCTTCGTACCAA 2700
881 HisHisLysGluLeuGluAlaProLeuIleProGlnArgThrHisSerLeuLeuTyrGln 900

2701 CCCCAGAAAGTGAAGTCCGAGGGAACGTGACAGCTATGTCTCCCACTGACAGCAGAG 2760
901 ProGlnLysLysValLysSerGluGlyThrAspSerTyrValSerGlnLeuThrAlaGlu 920

2761 GCTGAAGATCACCCTACAGTCCCCCAACAGAGACTCTCTTTATACAGCATGCCCAATCTT 2820
921 AlaGluAspHisLeuGlnSerProAsnArgAspSerLeuTyrThrSerMetProAsnLeu 940

2821 AGAGACTCTCCCTATCCGGAGAGCAGCCCTGACATGGAAGAAGACCTCTCTCCCTCCAGG 2880
941 ArgAspSerProTyrProGluSerSerProAspMetGluGluAspLeuSerProSerArg 960

2881 AGGAGTGAGATGAGGACATTTACTATATAAAGCANTGCCAAATCTTGAGCTGGCCATCAG 2940
961 ArgSerGluAsnGluAspIleTyrTyrLysSerMetProAsnLeuGlyAlaGlyHisGln 980

Figure 13

2941 CTTGAGATGTGCTACAGATCAGCAGGGCAATAGTATGTTATATATATCCCAITTAAC 3000
 981 LeuGlnMetCysTyrGlnIleSerArgGlyAsnSerAspGlyTyrIleIleProIleAsn 1000

 3001 AAAGAAGGGTGTATTCCAGAAGGAGATGTTAGAGAAGGACAAATGCCAGCTGTTACAAGT 3060
 1001 LysGluGlyCysIleProGluGlyAspValArgGluGlyGlnMetGlnLeuValThrSer 1020

 3061 CTTTAATCATACAGCTAAGGANTTCCAAGGGCCACATGCCGAGTATTAATAATAAGACA 3120
 1021 Leu*** 1022

 3121 CCAATGGCCTGACGCGAGCTCCCTCAAACTCTGCTTGAAGAGATGACTCTGACCTGTGGT 3180
 1022 1022

 3181 TCTCTGGTGTAATAAAGATGACTGAACCTTCCAGTTCCTGGAATTTTATAAAACATACA 3240
 1022 1022

 3241 AAAACTTTGTATATACACAGATGATTAATAAGTGAATTTTGTACAAAGAAAGAGAT 3300
 1022 1022

 3301 GCCAGCCAGGTATTTTAAGATTCCTGCTGCTGTTAGAGAAATGTGAACAAGCAAAACA 3360
 1022 1022

 3361 AAACCTTCCAGCCATTTTACTGCGCAGGAGTCTGTGAACTAAATTTGTAAATATGCGTGCAC 3420
 1022 1022

Figure 14

3421	CATTTTGTAGGCCTGCAATTCATATATACAAAGCGTAGGCCTTAAATCCCTGTTGGAC	3480
1022		1022
3481	AAATTTACTGTACCTTACTATTCCTGACAGACITGGAAAGCAGAGAGATATTCCTGCA	3540
1022		1022
3541	TCAGTTGCAGTTCACGCAATCTTTTACATTAGGCAAGATTCGAAACATGCTTAAC	3600
1022		1022
3601	CACTAGCAATCAAGCCACAGGCCCTTATTTTCATATGTTTCTCACTGTACATGAACCTAT	3660
1022		1022
3661	TCTCATGAAATGGCTAAGAAATATATTTTGTCTATTGCTAGGGTAAATATAATAC	3720
1022		1022
3721	ATTGTGTCCAACTGAAATATATATGTCATTAAATAATTTTAAAGAGTGAAGAAATAT	3780
1022		1022
3781	TGTGAAAGCTCTGTGGTGCACATGTTATGAATGTTTCTTACACTTTGTCTATGGTA	3840
1022		1022
3841	AGTTCTACTCATTTTCACTTCTTTTCCACGTATATACAGTGTCTGCTTTGACAAAGTTAG	3900
1022		1022
3901	TCTTTTATTACTTACATTTAAATTTCTTATTCGCAAAAGAACGTTGTTTATGGGAGAAAC	3960

Figure 15

1022
1022
3961 AAACCTCTTTGAAGCCAGTTAAGTCATCCCTTGACAAAGTGAAGAATCTAGAAAAGAT 4020
1022
4021 TGTGTGTCACCCCTGTTTATTCTTGAACAGAGGGCAAGAGGGCACATGGGCACCTTCTCAC 4080
1022
4081 AAACCTTTCTAGTGAACAAAAGGTGCCCTATTCTTTTAAAAAATAAATAAACATAAA 4140
1022
4141 TATTACTCTTCCATANTTCCCTTCGCTATATTAGTAATTAATTTATGATAAAGT 4200
1022
4201 TCTAATGAANTGTAAATGTGTTTCAGCAAAATCTGCTTTTTTTTTCATCCCTTTTGTTAAA 4260
1022
4261 CCTGTAAATAATGAGCCCATCACTAATATCCAGTGTAAAGTTTAAACACGGTTTGACAGTA 4320
1022
4321 AATAAATGTGAATTTTTCAGT 4343
1022

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Figure 16

	1				50
HK05006					
HK05490					
HH02631	MARLA AVLWN	LCVTAVLVTS	ATQGLSRAGL	PFGLMRRELA	CEGYPIELRC
	51				100
HK05006					
HK05490					
HH02631	PGSDVIMVEN	ANYGRTDDKI	CDADPFQMEN	VQCYLPDAFK	IMSQR CNNRT
	101				150
HK05006					
HK05490					
HH02631	QCVVVAGSDA	FPDPCPGTYK	YLEVQYDCVP	YKVEQKVFVC	PGTLQKVLEP
	151				200
HK05006					
HK05490					
HH02631	TSTHESEHQS	GAWCKDPLQA	GDRIYVMPWI	PYRTDTLTEY	ASWEDYVAAR
	201				250
HK05006					
HK05490					
HH02631	HTTTYRLPNR	VDGTGFVVYD	GAVFYNKERT	RNIVKYDLRT	RIKSGETVIN
	251				300
HK05006					
HK05490					
HH02631	TANYHDTSPY	RWGGKTDIDL	AVDENGLWVI	YATEGNNGRL	VVSQ LNPYTL
	301				350
HK05006					
HK05490					
HH02631	RFEGTWETGY	DKRSASNAFM	VCGVLYVLRS	VYVDDDSEAA	GNRVDYAFNT

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Figure 17

	351				400
HK05006	_____	_____	_____	_____	_____
HK05490	_____	_____	_____	_____	_____
HH02631	NANREEPVSL	TFPNPYQFIS	SVDYNPRDNQ	LYVWNNYFVV	RYSLEFGPPD
	401				450
HK05006	_____	_____	_____	_____	_____
HK05490	_____	_____	_____	_____	E
HH02631	PSAGPATSP	LSTTTTARPT	PLTSTASPAA	TTPLRRAPLT	THPVGAINQL
	451				500
HK05006	_____	_____	_____	_____	_____
HK05490	GSKGTPPPA	VSTTKIPPIT	NIFPLPERFC	EALDSKGIKW	PQTQRGMMVE
HH02631	GPLPAPATAP	VPSTRRPPAP	NLHVSPFLC	EPREVRVQW	PATQQGMLVE
	501				550
HK05006	_____	_____	_____	_____	_____
HK05490	RPCPKGTRGT	ASYLCMISTG	TWNPKGPDLS	NCTSHWVNQL	AQKIRSGENA
HH02631	RPCPKGTRGI	ASFQCLPALG	LWNPRGPDLS	NCTSPWVNQV	AQKIKSGENA
	551				600
HK05006	_____	AEQ	TRNHLNAGDI	TYSVRAMDQL	VGLLDVQLRN
HK05490	ASLANELAKH	TKGPVFAGDV	SSSVRLMEQL	VDILDAQLQE	LKPSEKDSAG
HH02631	ANIASELARH	TRGSIYAGDV	SSSVKLMEQL	LDILDAQLQA	LRPIERESAG
	601				650
HK05006	RSLN. KAM	VETVNNLLQP	QALNAWRDLT	TSDQLRAATM
HK05490	RSYNKLQKRE	KTCRAYLKAI	VDTVNDLLRP	EALSWKHMN	SSEQAHTATM
HH02631	KNYNKMHKRE	RTCKDYIKAV	VETVDNLLRP	EALSWKDMN	ATEQVHTATM
	651				700
HK05006	LLHTVEESAF	VLADNLLKTD	IVRENTDNIK	LEVARLSTEG	NLEDLKFP. E
HK05490	LLDTLEEGAF	VLADNLLIPT	RVSMTPTENIV	LEVAVLSTEG	QIQDFKFLPG
HH02631	LLDVLEEGAF	LLADNVREPA	RFLAAKENVV	LEVTVLNTEG	QVQELVFPQE

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Figure 18

	701		750
HK05006	NMGHGSTIQL	SANTLKQNGR	NGEIRVAFVL YNNLGPYLST ENASMKLGTE
HK05490	IKGAGSSIQL	SANTVKQNSR	NGLAKLVFII YRSLGQFLST ENATIKLGAD
HH02631	EYPRKNSIQL	SAKTIKQNSR	NGVVKVVFIL YNNLGLFLST ENATVKLAGE
	751		800
HK05006	A...LSTNHS	VIVNSPVITA	AINKEFSNKV YLADPVVFTV KHIKQSEENF
HK05490	F...IGRNST	IAVNSHVISV	SINKE. SSRV YLTDPVLFTL PHI. DPDNYF
HH02631	AGPGGPGGAS	LVVNSQVIAA	SINKE. SSRV FLMDPVIFTV AHL. EDKNHF
	801		850
HK05006	NPNCSEFWSYS	KRTMTGYWST	QGCRLTTNK THHTCSCNHL TNFAVLMAHV
HK05490	NANCSFWNYS	ERTMMGYWST	QGCKLVDTNK TRTTCACSHL TNFAILMAHR
HH02631	NANCSFWNYS	ERSMLGYWST	QGCRLVESNK THHTCACSHL TNFAVLMAHR
	851		900
HK05006	EVKHSDAVHD	LLLDVITWVG	ILLSLVCLLI CIFTFCFFRG LQSDRNTIHK
HK05490	EIAYKDGVE	LLLTVITWVG	IVISLVCLAI CIFTFCFFRG LQSDRNTIHK
HH02631	EI. YQGRINE	LLLSVITWVG	IVISLVCLAI CISTFCFLRG LQTDNRNTIHK
	901		950
HK05006	NLCISLFVAE	LLFLIGINRT	DQPIACAVFA ALLHFFFLAA FTWMFLEGVQ
HK05490	NLCINLFIAE	FIFLIGIDKT	KYAIACPIFA GLLHFFFLAA FAWMCLEGVQ
HH02631	NLCINLFLAE	LLFLVGIDKT	QYEIACPIFA GLLHYFFLAA FSWLCLEGVH
	951		1000
HK05006	LYIMLVEVFE	SEHSRRKYFY	LVGYGMPALI VAVSAAVDYR SYGTDKVCWL
HK05490	LYLMLVEVFE	SEYSRKKYYY	VAGYLFPATV VGVSAAIDYK SYGTEKACWL
HH02631	LYLLLVEVFE	SEYSRTKYYY	LGGYCFPALV VGIAAAIDYR SYGTEKACWL
	1001		1050
HK05006	RLDTYFIWSF	IGPATLIIML	NVIFLGIALY KMFHHTAILK PESGCLDNIK
HK05490	HVDNYFIWSF	IGPVTFIILL	NIIFLVITLC KMKVHSNTLK PDSSRLENIK
HH02631	RVDNYFIWSF	IGPVSVFIVV	NLVFLMVTLH KMIRSSSVLK PDSSRLDNIK

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Figure 19

	1051	1100
HK05006	SWVIGAIALL CLLGLTWAFG LMYINESTVI MAYLFTIFNS LQGMFIFIFH	
HK05490	SWVLGAFALL CLLGLTWSFG LLFINEETIV MAYLFTIFNA FQGVFIFIFH	
HH02631	SWALGAIALL FLLGLTWAFG LLFINKESVV MAYLFTTFNA FQGVFIFVFH	
	1101	1150
HK05006	CVLQKKVRKE YGKCLR. THC CSGKSTESSI GSGKTSGSRT PGRYSTGSQS	
HK05490	CALQKKVRKE YGKCFRHSYC CGGLPTESPH SSVKASTTRT SARYSSGTQS	
HH02631	CALQKKVHKE YSKCLRHSYC CIRSPPGGTH GSLKTSAMRS NTRYTGTQS	
	1151	1200
HK05006	RIRRMWNDTV RKQSESSFIT GDINSSASLN REGLLN.	
HK05490	RIRRMWNDTV RKQSESSFIS GDINSTSTLN QGMTGNYLLT NPLLPHGTN	
HH02631	RIRRMWNDTV RKQTESSFMA GDINSTPTLN RGTMGNHLLT NPVLQPRGGT	
	1201	1250
HK05006 NARDTS VMDTLPLNGN	
HK05490	NPYNTLLAET VVCNAPSAPV FNSPGHSLN. NARDTS AMDTLPLNGN	
HH02631	SPYNTLIAES VGFNPSSPPV FNSPGSYREP KHPLGGREAC GMDTLPLNGN	
	1251	1300
HK05006	HGNSYSIASG EYLSN. CVQI IDRGYNHNE. TALEKKILKE LTSNYIPSYL	
HK05490	FNNSYSLHKG DY. . NDSVQV VDCGLSLND. TAFEKMIISE LVHN. ... NL	
HH02631	FNNSYSLRSG DFPPGDDGPE PPRGRNLADA AAFEKMIISE LVHN. ... NL	
	1301	1350
HK05006	NNHERSSEQN RNLMNKLVNN LGSGREDDAI VLDDATSFNH EESLGLELIH	
HK05490	RGSSKTHN. . LELTLPVKPV IGGSSSEDDA IVADASSLMH SDNPGLELHH	
HH02631	RGSSSAAKGP PPPEPPVPPV PGGGGEE. ... EAGGPGG ADRAEIELLY	
	1351	1400
HK05006	EESDAPLLPP RYVSTENHQP HHYTRRRIPQ DHSSEFFPLL TNEHTEDLQS	
HK05490	KELEAPLIPQ RTHSL. LYQPQKKVKS EGTDSYVSQ L TAEADHLQS	
HH02631	KALEEPLLLP RAQSV. LYQSD. ... L DESESCAED GATSRPLSSP	

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Figure 20

1401 1450
HK05006 PHRDSLYTSM PTLAGVAATE SVTTSTQTE. . . PPPAKCGD AEDVYYKSM.
HK05490 PNRDSLYTSM PNLRDSP. YP ESSPDMEEDL . . . SPSRRSE NEDIYYKSM.
HH02631 PGRDSLYASG ANLRDSPSYP DSSPEGPSEA LPPPPPAPPG PPEIYYTSRP

1451 1500
HK05006 PNLGSRNHVH QLHTYYQLGR GSSDGFIVPP NKDGTPEGS . SKGPAHLVT
HK05490 PNLGAG. . . H QLQMCYQISR GNSDGYIPI NKEGCIPEGD VREGQMLVT
HH02631 PALVAR. . . N PLQGYQVRR PSHEGYLAAP GLEGPGPDGD . . . GQMQLVT

1501
HK05006 SL
HK05490 SL
HH02631 SL

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Figure 21

TTTTTTTTTTTTTTTTTTCTAATTTTTGGTCGGCGGCGGTGCTGGGCCAG 50
 GGGAAGGAAGGGACACGGAGGCCGCCCTCGTCCCGCCACCTCCTACCCGC 100
 TTCCCCCAGCCCCGGCTCCGGGAGATGTGCCGGGCGGGGGGCCCGGGTT 150
 CGCCGAGCCGCAGGAGAGACACGCTGGGCCGACCCCAGAGAGGCGCTGGA 200
 CAGGCTGGTGGTCCAGGCCGTGGTGCCTGCCAGGTGATGTGGGGCAAAGC 250
 CCCCCGCACAGGCCACTGAGAGCTCCGGACACGCACCCGGCTGCCACCAT 300
 GGCCCGCCTAGCCGCAGTGCTCTGGAATCTGTGTGTACCGCCGTCCTGG 350
 TCACCTCGGCCACCCAAGGCCTGAGCCGGGCCGGGCTCCCGTTCGGGCTG 400
 ATGCGCCGGGAGCTGGCGTGTGAAGGCTACCCCATCGAGCTGCGGTGCC 450
 CGGCAGCGACGTCATCATGGTGGAGAATGCCAACTACGGGCGCACGGACG 500
 ACAAGATTTGCGATGCTGACCCTTTCCAGATGGAGAATGTGCAGTGCTAC 550
 CTGCCGGACGCCTTCAAGATCATGTACAGAGGTGTAACAACCGCACCCA 600
 GTGCGTGGTGGTCCCGGCTCGGATGCCTTTCTGACCCCTGTCCTGGGA 650
 CCTACAAGTACCTGGAGGTGCAGTACGACTGTGTCCCCTACAAAGTGGAG 700
 CAGAAAGTCTTCGTGTGCCAGGGACCCTGCAGAAGGTGCTGGAGCCAC 750
 CTCGACACACGAGTCAGAGCACCACTGTGGCGCATGGTGCAAGGACCCGC 800
 TGCAGGCGGGTGACCGCATCTACGTGATGCCCTGGATCCCCTACCGCACG 850
 GACACACTGACTGAGTATGCCTCGTGGGAGGACTACGTGGCCGCCGCCA 900
 CACCACCACCTACCGCCTGCCCAACCGCGTGATGGCACAGGCTTTGTGG 950
 TCTACGATGGTGCCGTCTTCTACAACAAGGAGCGCACGCGCAACATCGTC 1000
 AAGTATGACCTACGGACGCGCATCAAGAGCGGGGAGACGGTCATCAATAC 1050
 CGCCAACCTACCATGACACCTCGCCCTACCGCTGGGGCGGAAAGACCGACA 1100
 TTGACCTGGCGGTGGACGAGAACGGGCTGTGGGTCTCTACGCCACTGAG 1150
 GGCAACAACGGGCGGCTGGTGGTGAGCCAGCTGAACCCCTACACACTGCG 1200
 CTTTGAGGGCACGTGGGAGACGGGTTACGACAAGCGCTCGGCATCCAACG 1250
 CCTTCATGGTGTGTGGGGTCTGTACGTCCTGCGCTCCGTGTACGTGGAT 1300
 GATGACAGCGAGGCGGCTGGCAACCGCGTGGACTATGCCTTCAACACCAA 1350
 TGCCAACCGCGAGGAGCCTGTCAGCCTCACCTTCCCCAACCCCTACCAGT 1400
 TCATCTCCTCCGTTGACTACAACCCTCGCGACAACCAGCTGTACGTCTGG 1450
 AACAACTATTTTCGTGGTGGCTACAGCCTGGAGTTCGGGCGGCCGACCC 1500
 CAGTGCTGGGCCAGCCACTTCCCCACCCCTCAGCACGACCACCACAGCCA 1550
 GGCCACGCCCCCTCACCAGCACAGCCTCGCCCGCAGCCACCACCCCGCTC 1600
 CGCCGGGCACCCCTCACCAGCACCCAGTGGGTGCCATCAACCAGCTGGG 1650
 ACCTGATCTGCCTCCAGCCACAGCCCCAGTCCCCAGCACCCGGCGGCCCC 1700
 CAGCCCCGAATCTACACGTGTCCCTGAGCTCTTCTGCGAGCCCCGAGAG 1750

Figure 22

GTACGGCGGGTCCAGTGGCCGGCCACCCAGCAGGGCATGCTGGTGGAGAG 1800
GCCCTGCCCCAAGGGGACTCGAGGAATTGCCTCCTTCCAGTGTCTACCAG 1850
CCTTGGGGCTCTGGAACCCCCGGGGCCCTGACCTCAGCAACTGCACCTCC 1900
CCCTGGGTCAACCAGGTGGCCGAGAAGATCAAGAGTGGGGAGAACGCGGC 1950
CAACATCGCCAGCGAGCTGGCCCGACACACCCGGGGCTCCATCTACGCGG 2000
GGGACGTCTCCTCCTCTGTGAAGCTGATGGAGCAGCTGCTGGACATCCTG 2050
GATGCCCAGCTGCAGGCCCTGCGGCCCATCGAGCGGAGTCAGCCGGCAA 2100
GAACTACAACAAGATGCACAAGCGAGAGAGAACTTGTAAGGATTATATCA 2150
AGGCCGTGGTGGAGACAGTGGACAATCTGCTCCGGCCAGAAGCTCTGGAG 2200
TCCTGGAAGGACATGAATGCCACGGAGCAGGTGCACACGGCCACCATGCT 2250
CCTCGACGTCTGGAGGAGGGCGCCTTCTGCTGGCCGACAATGTCAGGG 2300
AGCCTGCCCCGCTTCTGGCTGCCAAGGAGAACGTGGTCTGGAGGTCACA 2350
GTCCTGAACACAGAGGGGCCAGGTGCAGGAGCTGGTGTTCCCCCAGGAGGA 2400
GTACCCGAGAAAGAACTCCATCCAGCTGTCTGCCAAAACCATCAAGCAGA 2450
ACAGCCGCAATGGGGTGGTCAAAGTTGTCTTCATCCTCTACAACAACCTG 2500
GGCCTCTTCTGTCCACGGAGAATGCCACAGTGAAGCTGGCCGGCGAAGC 2550
AGGCCCGGGTGGCCCTGGGGGCGCCTCTCTAGTGGTGAACCTCACAGGTCA 2600
TCGCAGCATCCATCAACAAGGAGTCCAGCCGCGTCTTCTCATGGACCCT 2650
GTCATCTTCACCGTGGCCACCTGGAGGACAAGAACCACTTCAATGCTAA 2700
CTGCTCCTTCTGGAAGTACTCGGAGCGTTCCATGCTGGGCTATTGGTGA 2750
CCCAAGGCTGCCGCCTGGTGGAGTCCAACAAGACCCATACCAGGTGTGCC 2800
TGCAGCCACCTACCAACTTCGCTGTGCTCATGGCTCACCGTGAGATCTA 2850
CCAGGGCCGCATCAACGAGCTGCTGCTGTGCGTGCATCACCTGGGTGGGCA 2900
TTGTGATCTCCCTGGTCTGCTTGGCCATCTGCATCTCCACCTTCTGCTTC 2950
CTGCGGGGGCTGCAGACCGACCGCAACACCATCCACAAGAACCTGTGCAT 3000
CAACCTCTTCTGGCTGAGCTGCTCTTCTGGTGGGATCGACAAGACTC 3050
AGTATGAGATTGCCTGCCCCATCTTCGCCGGCCTGCTGCACTATTTCTTC 3100
CTGGCTGCCTTCTCCTGGCTGTGCCTGGAGGGCGTGCACCTCTACCTGCT 3150
ACTAGTGGAGGTGTTTGAGAGCGAGTATTCCCGCACCAAGTACTACTACC 3200
TGGGTGGCTACTGCTTCCCGGCCCTGGTGGTGGGCATCGCGGCTGCCATT 3250
GACTACCGCAGCTACGGCACCGAGAAGGCCTGCTGGCTCCGAGTGGACAA 3300
TTACTTCATCTGGAGTTTCATCGGGCCAGTCTCCTTCGTTATCGTGGTCA 3350
ACCTGGTGTTCTCATGGTGACCCTGCACAAGATGATCCGAAGCTCATGT 3400
GTGCTCAAGCCCGACTCCAGCCGCCTGGACAACATTAAATCCTGGGCGCT 3450
GGGGGCCATCGCGCTGCTGTTCTGCTGGGCCTCACCTGGGCTTTCGGCC 3500

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Figure 23

TCCTCTTCATCAACAAGGAGTCGGTGGTCATGGCCTATCTCTTCACCACC 3550
TTCAACGCCTTCCAGGGGGTCTTCATCTTCGTCTTTCACTGCGCCTTACA 3600
GAAGAAGGTGCACAAGGAGTACAGCAAGTGCCTGCGTCACTCCTACTGCT 3650
GCATCCGCTCCCCACCCGGGGGCACTCACGGATCCCTCAAGACCTCAGCC 3700
ATGCGAAGCAACACCCGCTACTACACAGGGACCCAGAGCCGAATTTCGGAG 3750
GATGTGGAATGACACTGTGAGGAAACAGACGGAGTCCTCCTTCATGGCGG 3800
GTGACATCAACAGCACCCCCACCCTGAACCGAGGTACCATGGGGAACCAC 3850
CTGCTGACCAACCCCGTGCTGCAGCCCCGTGGGGGCACCAGTCCCTACAA 3900
CACCCCTCATCGCCGAGTCAGTGGGCTTCAATCCCTCCTCGCCCCCTGTCT 3950
TCAACTCCCCAGGGAGCTACCGGGAACCCAAGCACCCCTTGGGAGGCCGG 4000
GAAGCCTGTGGCATGGACACCCTGCCCCTGAACGGCAACTTCAATAACAG 4050
TACTCCTTGCGAAGTGGGGATTTCCCTCCCGGGGATGGGGGCCCTGAGC 4100
CGCCCCGAGGCCGGAACCTAGCCGATGGGGCGGCCTTTGAGAAGATGATC 4150
ATCTCAGAGCTGGTGCACAACAACCTGCGGGGGAGCAGCAGCGCGGCCAA 4200
GGGCCCTCCACCGCCTGAGCCCCCTGTGCCACCTGTGCCAGGGGGCGGGG 4250
GCGAGGAAGAGGCGGGCGGGCCCCGGGGGTGCTGACCGGGCCGAGATTGAA 4300
CTTCTCTATAAGGCCCTGGAGGAGCCTCTGCTGCTGCCCCGGGCCAGTC 4350
GGTGCTGTACCAGAGCGATCTGGACGAGTCGGAGAGCTGCACGGCCGAGG 4400
ACGGCGCCACCAGCCGGCCCCCTCTCCTCCCTCCTGGCCGGGACTCCCTC 4450
TATGCCAGCGGGGCCAACCTGCGGGACTCACCCCTCTACCCGGACAGCAG 4500
CCCTGAGGGGCCCAGTGAGGCCCTGCCCCACCCCTCCCGCACCCCCCG 4550
GCCCCCCCCGAAATCTACTACACCTCGCGCCCGCCAGCCCTGGTGGCCCGG 4600
AATCCCCTGCAGGGCTACTACCAGGTGCGGCGTCCTAGCCACGAGGGCTA 4650
CCTGGCAGCCCCAGGCCCTTGGGGGCCAGGGCCCGATGGGGACGGGCAGA 4700
TGCAGCTGGTCACCAGTCTCTGAGGGCACCTCATGGACCAGGGGCTGGTG 4750
GCCCAGGCCAGGGAGGGAACCTGGGCAGGGCTCTGGTGGGAGAGGGAGA 4800
CAGATGGAGGCAGTGGCTGGTGGGCCACTCTCTCCAGGTGCCCCCTCAGCC 4850
ATGGGCCCTACAGTCCCCTCAGGGGACTCTAACCTGGGGGCCTGAGGTGC 4900
CAGGGTTCACAGACAGGGTTTCCCACCAGCCACACGCACCAGCTCTATTT 4950
GGGGGAAGTGTAGTGAGGAGGAGCCAGAGGACCCAGGGGAGTGAGGAG 5000
GGAGAACTTGGAAGGGTGCAGCCCACTTCCAGACTCTCCCCTCTCCACC 5050
CTTCTACCTGTGAAGGGAAATGAGGGCTTTAGTTTCCTGGGCAGGGAGG 5100
GGCAGCTTCTGAGGTTGCCAAAGGCCCCCACTGGATGGAACCTGTTAGCT 5150
GCTCCTCTCCGCAGCCAGAAATGCTGCCGGCTGCACCCAGAGGGAGCAGT 5200
GAGGCAGGACAGATGGACAGGTTCTCCTGCGCTGTAATTCCTGCTCCC 5250

Figure 24

TGGAGACTGGGAAAAGGCCGCAGGGCAGGGGGACTGGGCGGTGGTGGCTG 5300
GTGGTTTAAAGGTTGAACTTTCTCTGAAGCTCCTTTCCCTTGCTCTTGG 5350
TCCCTGCCCCGCAAGCAAACCTGCCCCCTCTGCCTCCCAGTGCACCCAAT 5400
GACCCCTCCCTTGGGGCGACTCCTGATGAAGCACAACCTCCCCGCAGGGC 5450
CCCCAGCCCACAGGGGTGGCCATATTTGGGCAGTTCCCAGTCCTGTGGGC 5500
TCGGCTATCTGGGGAGCAGATTTTGGGTCTGGATCTCCCTGGGGAGTGGG 5550
TCCTGGGCTTGGATCTTCCCTAGGGGGCCCTCTTACTCCTTCCTCTCTC 5600
CTCCTCCTTCCCCATTGCTGTAAATATTTCAACGAAATGGAAAAGAAAAA 5650
AAAAAAGAC 5659

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Figure 25

